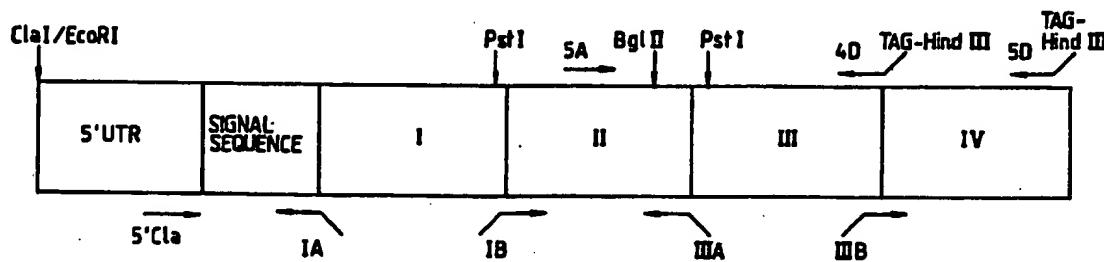




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(54) Title: MODIFIED HUMAN TNFALPHA (TUMOR NECROSIS FACTOR ALPHA) RECEPTOR



(57) Abstract

A polypeptide which is capable of binding human TNF α and which consists essentially of: a) the first three cysteine-rich subdomains, but not the fourth cysteine-rich subdomain, of the extracellular binding domain of the 55kD or 75kD receptor for human TNF α ; or b) an amino acid sequence having a homology of 90 % or more with the said sequence (a).

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Modified human TNFalpha (Tumor Necrosis Factor alpha) Receptor.

The present invention relates to recombinant proteins and their use.

Tumour necrosis factor- α (TNF α) is a potent cytokine which elicits a broad spectrum of biological responses. TNF α causes the cytolysis or cytostasis of many tumour cell lines *in vitro*, induces the haemorrhagic necrosis of transplanted tumours in mice, enhances the phagocytosis and cytotoxicity of polymorphonuclear neutrophils, and modulates the expression of many proteins, including lipoprotein lipase, class I antigens of the major histocompatibility complex, and cytokines such as interleukin 1 and interleukin 6. TNF α appears to be necessary for a normal immune response, but large quantities produce dramatic pathogenic effects. TNF α has been termed "cachectin" since it is the predominant factor responsible for the wasting syndrome (cachexia) associated with neoplastic disease and parasitemia. TNF is also a major contributor to toxicity in gram-negative sepsis, since antibodies against TNF can protect infected animals.

The many activities of TNF α are mediated by binding to a cell surface receptor. Radioligand binding studies have confirmed the presence of TNF receptors on a wide variety of cell types. Although these receptors are expressed in limited numbers (1,000 - 10,000 receptors/cell), they bind TNF α with high affinity ($K_a = 10^9 M^{-1}$ at 4°C). Lymphotoxin (LT, also termed TNF β) has similar, if not identical, biological activities to TNF α , presumably because both are recognized by the same receptor.

Recently, several laboratories have detected heterogeneity in TNF receptor preparations. Two distinct cell surface receptors which bind TNF α and TNF β have recently been characterised at the molecular level. cDNA for one form of the receptor with a Mr of 55kD was isolated utilising probes designed from the peptide sequence of a

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s luble form f the rec pt r (1,2). A second r c ptor of Mr 75kD was cl ned by a COS cell expr ssi n appr ach (3). Both receptors are members of a larger family of cytokine receptors which include the nerve growth factor receptor, 5 the B cell antigen CD40, the rat T cell antigen MRC OX40. In addition these receptors are homologous to the predicted product of a transcriptionally active open reading frame from shope fibroma virus which appears to give rise to a secreted protein.

10 The most conserved feature amongst this group of cell surface receptors is the cysteine rich extracellular ligand binding domain, which can be divided into four repeating motifs of about forty amino acids. We have now generated four soluble receptor derivatives of the 55kD TNF α receptor 15 (TNFR). Each derivative is composed of the extracellular binding domain but without one of the cysteine rich subdomains. We have found that the derivative which lacks the membrane-proximal fourth subdomain retains the ability to bind TNF α with high affinity. This finding has general 20 applicability.

Accordingly, the present invention provides a polypeptide which is capable of binding human TNF α and which consists essentially of:

(a) the first three cysteine-rich subdomains, but not 25 the fourth cysteine-rich subdomain, of the extracellular binding domain of the 55kD or 75kD receptor for human TNF α ; or

(b) an amino acid sequence having a homology of 90% or more with the said sequence (a).

30 The invention also provides:

- a DNA sequence which encodes such a polypeptide;
- a vector which incorporates a DNA sequence of the invention and which is capable, when provided in a transformed host, of expressing the polypeptide of the 35 invention encoded by the DNA sequence; and

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a host transformed with such a vector.

In the accompanying drawings:

Figure 1 shows the nucleotide sequence of the human TNF α cDNA and encoded amino acid sequence. The predicted signal

5 sequence residues are numbered -40 to -1. The transmembrane domain is boxed and potential N-linked glycosylation sites are overlined. The sequence homologous with the designed oligonucleotide probe is found at nucleotide positions 477-533.

10 Figure 2 is a Northern blot (lanes 1-3) of 10 μ g of oligo-dT selected RNA from human 293 cells (fibroblast cell line) (lane 1), placenta (lane 2) and spleen (lane 3) hybridised with the TNF receptor cDNA (SmaI-EcoRI fragment). The Southern blot (lanes 4-6) was hybridized
15 with the same probe. Human genomic DNA (5 μ g per lane) was digested with PstI (lane 4), Hind III (lane 5) and EcoRI (lane 6).

Figure 3 shows the binding characteristics of recombinant human TNF receptor expressed in COS-7 cells.

20 The direct binding of recombinant 125 I-TNF α to COS-7 cells transfected with pRTNFR is presented in panel A. The inset contains Scatchard analysis derived from this data. As shown in panel B, monolayers of Cos-7 cells transfected with TNFR cDNA were incubated with 1nM 125 I-TNF in the
25 presence of various concentrations of unlabelled TNF α or TNF β .

Figure 4 shows the effects of soluble TNFR on TNF α binding and biological activity. Panel A shows the effects of supernatants from Cos-7 cells transfected with a cDNA
30 encoding a soluble form of the TNF receptor (pTNFRecd, closed circles) or mock transfected (open circles) on 125 I-TNF binding to U937 cells. Panel B shows the effects of these supernatants on TNF mediated killing of WEHI 164 (clone 13) line. Assays were performed as described in
35 Materials and Methods.

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Figure 5 is a diagram of the DNA sequence of pTNFRecd and is also a strategy map for polymerase chain reaction (PCR)-based domain deletion, in which 5'UTR is the 5'-untranslated region and I to IV are the four cysteine-rich 5 subdomains. The oligonucleotides employed in PCR in the Example and relevant restriction sites are also shown.

Figure 6 shows lined up the amino acid sequences of the four cysteine-rich subdomains of the 55kD (TNFR-55) and 75kD (TNFR-75) receptors and of rat nerve growth factor 10 receptor (NGFR), human CD40 and rat OX40. Homology is shown by means of boxes.

Figures 7 to 11 show the nucleotide sequence and the predicted amino acid sequence of the encoded polypeptide of pTNFRecd, pΔI, pΔII, pΔIII and pΔIV.

15 Figure 12 shows the results of the assays described in the Example 1.

Figure 13 shows diagrammatically the DNA encoding the 75kD receptor in which I to IV are the four cysteine-rich 20 subdomains. Oligonucleotides employed in PCR-domain deletion are also shown.

A polypeptide according to the invention is capable of binding human TNF α . Typically the polypeptide has a binding affinity for human TNF α of $10^7 M^{-1}$ or greater, for example $10^8 M^{-1}$ or greater. The affinity may be from 10^7 to 25 $10^{10} M^{-1}$, for example from 10^8 to $10^9 M^{-1}$.

A preferred polypeptide consists essentially of the first three cysteine-rich subdomains of the extracellular binding domain of the 55kD receptor for human TNF α . The sequence (a₁) of these three subdomains is:

V	C	P	Q	G															
K	Y	I	H	P	Q	N	N	S	I	C	C	T	K	C	H	K	G	T	Y
L	Y	N	D	C	P	G	P	G	Q	D	T	D	C	R	E	C	E	S	G
S	F	T	A	S	E	N	H	L	R	H	C	L	S	C	S	K	C	R	K
E	M	G	Q	V	E	I	S	S	C	T	V	D	R	D	T	V	C	G	C
R	K	N	Q	Y	R	H	Y	W	S	E	N	L	F	Q	C	F	N	C	S
35	L	C	L	N	G	T	V	H	L	S	C	Q	E	K	Q	N	T	V	C.

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A useful polypeptide has the amino acid sequence (c):

M	G	L	S	T	V	P	D	L	L	L	P	L	V	L	L	E	L	L	V	
G	I	Y	P	S	G	V	I	G	L	V	P	H	L	G	D	R	E	K	R	
D	S	V	C	P	Q	G	K	Y	I	H	P	Q	N	N	S	I	C	C	T	
5	K	C	H	K	G	T	Y	L	Y	N	D	C	P	G	P	G	Q	D	T	D
	C	R	E	C	E	S	G	S	F	T	A	S	E	N	H	L	R	H	C	L
	S	C	S	K	C	R	K	E	M	G	Q	V	E	I	S	S	C	T	V	D
	R	D	T	V	C	G	C	R	K	N	Q	Y	R	H	Y	W	S	E	N	L
	F	Q	C	F	N	C	S	L	C	L	N	G	T	V	H	L	S	C	Q	E
10	K	Q	N	T	V	C	T													

10 K Q N T V C T.

In an alternative embodiment, the polypeptide may consist essentially of the first three cysteine-rich subdomains of the extracellular binding domain of the 75kD receptor.

15 Apart from the amino acid sequence (a), the polypeptides may alternatively consist essentially of an amino acid sequence (b) having a homology of 90% or more with sequence (a). The degree of homology may be 95% or more or 98% or more. Amino acid sequence (a) may therefore be modified by

20 one or more amino acid substitutions, insertions and/or deletions and/or by an extension at either or each end. There should be no modification of the cysteine-residues, however. A polypeptide comprising sequence (b) must of course still be capable of binding human TNFa.

25 For example, one or more amino acid residues of the sequence (a), other than a cysteine residue, may be substituted or deleted or one or more additional amino acid residues may be inserted; provided the physicochemical character of the original sequence is preserved, i.e. in

30 terms of charge density, hydrophobicity/hydrophilicity, size and configuration. Conservative substitutions may be made. Candidate substitutions are, based on the one-letter code (Eur. J. Biochem. 138, 9-37, 1984):

35 A for G and vice versa,

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V by A, L or G;
K by R;
S by T and vice versa;
E for D and vice versa; and
5 Q by N and vice versa.

Up to 15 residues may be deleted from the N-terminal and/or C-terminal of the polypeptide, for example up to 11 residues or up to 5 residues.

The polypeptides of the invention consist essentially of
10 sequence (a) or (b). They do not contain a fourth cysteine-rich subdomain. However, the polypeptides may be longer polypeptides of which sequence (a) or (b) is a part. A short sequence of up to 50 amino acid residues may be provided at either or each terminal of sequence (a) or (b).
15 The sequence may have up to 30, for example up to 20 or up to 10, amino acid residues.

Alternatively, a much longer extension may be present at either or each terminal of sequence (a) or (b) of up to, for example, 100 or 200 amino acid residues. Longer amino acid sequences may be fused to either or each end. A chimaeric protein may be provided in which the or each extension is a heterologous amino acid sequence, i.e. a sequence not naturally linked to the amino acid sequence above. Such a chimaeric protein may therefore combine the 25 ability to bind specifically to human TNF α with another functionality.

The polypeptides of the invention lack the fourth cysteine-rich subdomain of the 55kD or 75kD receptor as the case may be. In particular, they lack the cysteine 30 residues of the fourth subdomain. They therefore do not comprise, immediately after the third cysteine-rich subdomain, any of the amino acid sequence up to the last cysteine residue of the fourth cysteine-rich subdomain of the relevant receptor except possibly the first amino acid 35 residue of that sequence. The polypeptides may extend

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TGC TGT ACC AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC TGT
CCA GGC CCG GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC GGC
TCC TTC ACC GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC
TCC AAA TGC CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC
5 ACA GTG GAC CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC
CGG CAT TAT TGG AGT GAA AAC CTT TTC CAG TGC TTC AAT TGC AGC
CTC TGC CTC AAT GGG ACC GTG CAC CTC TCC TGC CAG GAG AAA CAG
AAC ACC GTG TGC ACC.

A DNA sequence encoding a polypeptide of the invention
10 may be synthesised. Alternatively, it may be constructed
by isolating a DNA sequence encoding the 55kD or 75kD
receptor from a gene library and deleting DNA downstream of
the coding sequence for the first three cysteine-rich
subdomains of the extracellular binding domain of the
15 receptor. This gives DNA encoding the first three
subdomains of either receptor. As an intermediate step,
DNA encoding the entire or nearly the entire extracellular
binding domain may be isolated and digested to remove DNA
downstream of the coding sequence for the first three
20 subdomains.

A modified nucleotide sequence, for example encoding an
amino acid sequence (b), may be obtained by use of any
appropriate technique, including restriction with an
endonuclease, insertion of linkers, use of an exonuclease
25 and/or a polymerase and site-directed mutagenesis. Whether
a modified DNA sequence encodes a polypeptide of the
invention can be readily ascertained. The polypeptide
encoded by the sequence can be expressed in a suitable host
and tested for its ability to bind specifically human TNF α .

30 For expression of a polypeptide of the invention, an
expression vector is constructed. An expression vector is
prepared which comprises a DNA sequence encoding a
polypeptide of the invention and which is capable of
expressing the polypeptide when provided in a suitable
35 host. Appropriate transcriptional and translational

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c ntr 1 elements are provided, including a promoter for the DNA sequence, a transcriptional termination site, and translational start and stop codons. The DNA sequence is provided in the correct frame such as to enable expression 5 of the polypeptide to occur in a host compatible with the vector.

The expression vector is then provided in an appropriate host. Cells harbouring the vector are grown so as to enable expression to occur. The vector may be a plasmid or 10 a viral vector. Any appropriate host-vector system may be employed.

The transformed host may be a prokaryotic or eukaryotic host. A bacterial or yeast host may be employed, for example E. coli or S. cerevisiae. Insect cells can 15 alternatively be used, in which case a baculovirus expression system may be appropriate. As a further alternative, cells of a mammalian cell line, such as Chinese Hamster Ovary (CHO) Cells may be transformed. A polypeptide glycosylated at one, two or three of the sites 20 shown in Figure 1 can be obtained by suitable choice of the host cell culture.

The polypeptide of the invention can be isolated and purified. The N-terminal of the polypeptide may be heterogeneous due to processing of the translation product 25 within a cell or as the product is being secreted from a cell. A mixture of polypeptides according to the invention, having different N-termini, may therefore be obtained. The polypeptide is soluble.

The polypeptides of the invention have activity binding 30 human TNF α . This activity is indicative of the possible use of the polypeptides in the regulation of TNF α -mediated responses by binding and sequestering human TNF α , for example possible use in treatment of pulmonary diseases, septic shock, HIV infection, malaria, viral meningitis, 35 graft versus host reactions and autoimmun diseases such as

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rheumat id arthritis.

For this purpose, a p lyp ptide f th pr sent invention may be formulated in a pharmaceutical composition. The pharmaceutical composition also comprises a 5 pharmaceutically acceptable carrier or diluent.

The polypeptide of the invention may be administered to a patient by any convenient route. The choice of whether an oral route or a parenteral route, such as subcutaneous, intravenous or intramuscular administration, is adopted; of 10 the dose; and of the frequency of administration depends upon a variety of factors. These factors include the purpose of the administration, the age and weight of the patient being treated and the condition of the patient. Typically, however, the polypeptide is administered in an 15 amount of from 1 to 1000 µg per dose, more preferably from 10 to 100 µg per dose, for each route of administration.

The following Examples illustrate the invention. A Reference Example is provided.

REFERENCE EXAMPLE

20 1. Materials and Methods

Reagents

Recombinant human TNF α and TNF β were supplied as highly purified proteins derived from *E. coli*. The specific activities of these preparations were approximately 10^7 25 units/mg, as measured in the murine L929 cell cytotoxicity assay (4). The synthetic oligonucleotides were prepared by Oswel DNA Service (University of Edinburgh).

Isolation of TNF α 55kD receptor cDNA clones

The sequence of a peptide fragment (E M G Q V E I S S T 30 V D R D T V C G) of the TNF binding protein was used to design a synthetic oligonucleotide probe (5' AAG GAG ATG GGC CAG GTT GAG ATC TCT TCT ACT GTT GAC AAT GAC ACT GTG TGT GGC-3'). The 57-mer DNA pr be was labelled with ^{32}P and T4

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polynucleotid kinase (N w England Biolab, Bev rly, MA) and us d t screen a placenta cDNA library in gt10 (5,6). Approximately 800,000 phage were transferred to nitrocellulose filters and screened at reduced stringency

5 Filters were incubated for 2 hours at 42°C in 0.05M sodium phosphate, pH 6.5, 20% formamide, 0.75 M sodium chloride, 0.075 M sodium citrate, 1% polyvinyl pyrrolidone (Sigma, St Louis, MO), 1% Ficoll, 1% bovine serum albumin (Sigma), and 50 ng/ml sonicated salmon sperm DNA (Sigma).

10 The radiolabelled probe was then added to the filters (10^8 cpm/ml final concentration) which were hybridized for 16 hours. Filters were washed extensively in 0.06M sodium chloride, 0.006M sodium citrate, 1% SDS at 37°C and positive clones were identified by autoradiography. Ten

15 hybridizing clones were plaque purified (5) and cDNA insert size was determined by polyacrylamide gel electrophoresis of EcoRI digested phage DNA. The inserts of two cDNA clones were sequenced using the dideoxy chain termination technique (8).

20 Southern and Northern blot analysis

DNA was isolated from human lymphocytes by the method of Blin and Stafford (9) and used for Southern blot analysis (10). DNA was digested with restriction endonucleases (New England Biolabs), fractionated on a 1% agarose gel, and

25 transferred to nitrocellulose. Hybridization and washing were conducted under stringent conditions (6) using a ^{32}P -labelled preparation of a 600 bp fragment of the TNF receptor cDNA. Northern blot analysis was performed (11) on oligo-dT selected RNA isolated from human placenta,

30 spleen (generously provided by the Cooperative Human Tissue Network, Birmingham, AL) and a fibroblast cell line (293 cells). Following electrophoresis on a formaldehyde 1.2% agarose gel, the RNA was transferred to nitrocellulose and hybridized with the TNF α rec ptor DNA prob under stringent

35 c nditions.

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Mammalian cell expression of the human TNF α 55kD receptor and derivatives

The coding region of the majority of the human TNF α 55kD receptor was isolated as an EcoRI fragment and cloned into 5 a mammalian cell expression vector (12), resulting in plasmid prTNFR. The EcoRI fragment encodes 374 amino acids of the TNF receptor; the 81 carboxyl terminal residues of the cytoplasmic domain are therefore missing from this plasmid construction. A derivative of the TNF α receptor 10 was produced by engineering a termination codon just prior to the transmembrane domain. The polymerase chain reaction (PCR) technique (13) was used to generate a 300 bp restriction fragment containing a BgIII site at the 5' end and a HindIII site preceded by a TAG stop codon at the 3' 15 end. The PCR primers were 5'GCTGCTCCAAATGCCGAAAG and 5'AGTTCAAGCTTTACAGTGCCCTAACATTCTAA.

The PCR product was gel purified and cloned into the TNF receptor expression plasmid (described above) digested with BgIII and HindIII. DNA sequencing confirmed that the 20 resulting plasmid (pTNFRecd) contained the designed DNA sequence. E. coli harbouring pTNFRecd were deposited at the National Collection of Industrial and Marine Bacteria, Aberdeen, GB on 11 September 1990 under accession number NCIMB 40315.

25 The TNF α receptor expression plasmids were transfected into monkey COS-7 cells using Lipofectin (Gibco BRL, Bethesda, MD) according to the manufacturer's instructions. Cells were cultured in Dulbecco's modified Eagle's medium containing 10% fetal calf serum.

30 Analysis of recombinant TNF α 55kD receptor derivatives

TNF α was radioiodinated with the Iodogen method (Pierce) according to the manufacturer's directions. The specific activity of the ^{125}I -TNF α was 10-30 $\mu\text{Ci}/\mu\text{g}$. COS c 11s

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transfected with the TNF α receptor cDNA (pTNFR, 1300 bp EcoRI fragment) were incubated for 24 hours and then seeded into six well tissue culture plates (Nunc) at 4.5×10^8 cells per well. The cells were incubated for a further 48

5 hours and then receptor expression was quantitated by radioligand binding for 2 hours at 4°C. Non-specific binding of ^{125}I -TNF α was determined in the presence of a 1,000 fold molar excess of unlabelled TNF α . Binding data was analysed by the method of Scatchard (14).

10 The TNF α receptor derivative was analysed for inhibition of ^{125}I -TNF α binding to the natural receptor on human U937 cells. Culture supernatant was harvested 72 hours after COS cells were transfected with pTNFRecd. U937 cells (2×10^8 cells in 200 μl) were incubated with 1nM ^{125}I -TNF α and

15 dilutions of COS cell media for 2 hours at 4°C. Cells were then centrifuged through 20% sucrose to remove unbound TNF α . Non-specific binding was determined in the presence of 1 μM unlabelled TNF α .

The TNF α receptor derivative was also analyzed for

20 inhibition of TNF α cytotoxic effects in vitro. The cytotoxicity assay was performed as described on the TNF sensitive cell line WEHI 164 clone 13 (15). Serial dilutions of supernatants from COS cells transfected with pTNFRecd or mock transfected controls were incubated with a

25 constant amount of TNF α (1 ng/ml) for 1 hour at 27°C before addition to the assay.

2. RESULTS

Isolation and characterization of the TNF α 55kD receptor cDNA

30 A partial amino acid sequence of the TNF binding protein was used to design a synthetic oligonucleotide probe. The radiolabelled probe was used to screen a human placenta cDNA library in lambda gt10 and ten hybridizing phage were isolated. The nucleotide and deduced amino acid sequences

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of the longest cDNA clone are depicted in Figure 1. The third potential ATG initiation codon occurs at position 156 of the nucleotide sequence; the first two ATG codons are closely followed by termination codons, and the third ATG 5 is preceded by the best translation initiation consensus nucleotides (16). The cDNA encodes an open reading frame of 1365 bases which codes for a polypeptide of 455 residues. Both of the peptide sequences determined by amino acid sequencing were identified in the encoded cDNA 10 (17 of 19 and 18 of 19 matching residues). The amino terminal end identified for the TNF binding protein corresponds to the cDNA encoded sequence beginning at residue 41. The first 35 amino acids are generally quite hydrophobic and probably represent a signal sequence. 15 Residues 35-40 are highly charged (DREKR) and such a sequence is not typically found in secretory signal sequences (17); perhaps the natural receptor is processed by proteolysis after residue 40 which contains a dibasic cleavage site (KR). Hydropathy analysis of the protein 20 sequence predicts a single transmembrane domain of 23 amino acids. This hydrophobic sequence divides the protein into an extracellular domain of 171 residues and a cytoplasmic domain of 221 residues. The amino acid composition determined for the TNF binding protein corresponds well 25 with the predicted composition of the extracellular domain encoded by the cDNA (results not shown). The discrepancy between the predicted receptor size (40,000 daltons) and the size determined by SDS-polyacrylamide gel electrophoresis (65,000 daltons, 18-20) is probably due to 30 glycosylation; there are four potential N-linked glycosylation sites in the sequence, three of which are in the extracellular domain. The sequence contains a large number (17) of cysteine residues, 24 of which are in the extracellular domain. The arrangement of these cysteine 35 residues is similar to that of several other cell surface

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proteins, suggesting that the TNF receptor is structurally related to a family of receptors.

A Northern blot analysis is presented in Figure 2. The ^{32}P -labelled cDNA hybridized to a single predominant band of oligo-dT selected RNA from human placenta or spleen. A minor larger transcript was also observed in RNA from a fibroblast cell line. The size of the hybridizing species is 2400 bases, in good agreement with the size of isolated cDNA. Also shown in Figure 2 is a Southern blot of human genomic DNA hybridized with a 600 bp probe from the cDNA. In each of the three different restriction digests, only a single hybridized signal was observed. Thus the TNF receptor that we have isolated appears to be encoded by a single gene.

15

Expression of recombinant TNF receptor sequences in mammalian cells

To confirm that the cDNA shown in Figure 1 indeed encodes the TNF receptor, the cDNA was engineered for expression in mammalian cells. The cDNA contains an EcoRI site at position 1270 of Figure 1. The receptor coding sequence was isolated as a 1300 bp EcoRI-fragment (containing all but the last 81 codons of the cytoplasmic domain) and inserted into a mammalian cell expression vector containing a cytomegalovirus promoter and SV40 transcription termination sequences (12). The resulting plasmid was transfected into COS cells which were analyzed for TNF receptor expression after three days. As shown in Figure 3, the transfected cells specifically bound radioiodinated TNF α in a saturable and dose dependent fashion. The population of COS cells expressed approximately 1×10^8 receptors per cell. The measured binding affinity of recombinant receptors was $2.5 \times 10^9 \text{ M}^{-1}$ at 4°C which is in close agreement with natural receptor in human cells (19,20). The binding of ^{125}I -TNF α (1 nM) to

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thes c lls could be inhibit d by th additi n of unlabelled TNF α r lymphot xin (Figure 3b). COS cells transfected with just the expression vector did not significantly bind ^{125}I -TNF α (less than 2% of the binding seen with the cDNA transfection).

The extracellular domain of the TNF receptor is naturally shed from cells. To produce a similar recombinant derivative, a stop codon preceding the transmembrane domain was engineered into the cDNA by PCR 10 mutagenesis. The modified DNA was inserted into the expression plasmid and subsequently transfected into cos cells. After three days, the COS cell media was tested for inhibition of TNF α binding to human U937 cells. As shown in Figure 4a, the transfected cell media inhibited up to 15 70% of the binding of TNF α . The recombinant TNF receptor derivative was next tested for inhibition of TNF α biological activity. A sensitive bioassay for TNF α is a measurement of cytolysis of mouse WEHI 164 (clone 13) cells. The transfected cell media inhibited 60% of TNF α 20 cytotoxicity on this cell line (Figure 4b). Media from mock transfected COS cells did not inhibit TNF α induced cytotoxicity or binding. These experiments demonstrate that the recombinant extracellular domain of the TNF receptor is capable of binding TNF and inhibiting its 25 biological activity.

EXAMPLE 1: Expression of polypeptide consisting essentially of the first three cysteine-rich subdomains of the extracellular binding domain of the 55kD receptor

1. MATERIALS AND METHODS

30 Reagents

E. coli derived recombinant human TNF α had a specific activity of 2×10^7 U/mg in an L929 cytotoxicity assay. Oligonucleotides were purchased from Oswel DNA service (University f Edinburgh).

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Generation of the recombinant soluble TNFR derivatives

Deletion of each of the subdomains in the recombinant soluble TNFR was achieved by means of PCR fragment joining and PCR mutagenesis. The sequence of the oligonucleotides used in these experiments is given in Table 1 and their locations relative to the four cysteine rich subdomains is shown in Figure 5. The four subdomains are lined up with respect to one another in Figure 6.

The plasmid pTNFRecd (Reference Example) is shown in Figure 7. pTNFRecd was further modified to remove 5' untranslated sequences by cloning of the Cla I/Bgl II digested product of a PCR using oligos 5' Cla and IIIA into ClaI/Bgl II digested pTNFRecd, to generate 5'-Δ Cla. Digestion of 5'-Δ Cla with Pst-1 and religation resulted in the generation of pΔII, which lacks the second cysteine rich subdomain (Figure 9). The fourth cysteine rich subdomain was removed by cloning of the BglIII/Hind III digested product of a PCR using oligonucleotides 5A and 4D into BglIII/Hind III 5'-Δ Cla; this introduced a termination codon after amino acid 167 (counting from the initial methionine) to yield pΔIV (Figure 11). The constructs p I (Figure 8) and pΔIII (Figure 10) which lack the first and third cysteine rich subdomains respectively were generated by joining PCR fragments by means of overlaps introduced into the primers used for the PCR. The gel purified products of PCR's using 5' Cla and IA and IB and 5D were mixed and subjected to further amplification using 5'Cla and 5D as primers. The resulting fragment was digested with ClaI and BglIII and cloned into ClaI/BglII digested pTNFRecd, to yield pΔI.

Similarly the gel purified products of PCR's using 5' Cla and IIIA and IIIB and 5D were mixed and subjected to further amplification using 5'Cla and 5D as primers. This product was digested with BglII and HindIII and cloned into Bgl II/Hind III cut 5'-Δ Cla to yield pΔIII. In all cases

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the cloned derivatives were analysed by restriction enzyme analysis and DNA sequencing using Sequenase (United States Biochemical Corporation).

Table 1: Structure of the mutagenic oligonucleotides

5	Oligo	<u>Sequence</u>
	<u>Name</u>	
	5'Cla	5'-GTTCTATCGATAAGAGGCCATAGCTGTCTGGC-3'
	IA	5'-GCTCTCACACTCTCTCTCCCTGTCCCCTAG-3'
	IB	5'-AGGGAGAAGAGAGAGTGTGAGAGCGGCTCCTTC-3'
10	IIIA	5'-TGCATGGCAGGTACACACGGTGTCCGGTCCAC-3'
	IIIB	5'-GACACCGTGTGTACCTGCCATGCAGGTTCTT-3'
	4D	5'-GGCCAAGCTTCAGGTGCACACGGTGTCTG-3'
	5A	5'-GCTGCTCCAAATGCCGAAAG-3'
	5D	5'-AGTTCAAGCTTTACAGTGCCCTAACATTCTAA-3'

15 Analysis of recombinant soluble TNFR derivatives

COS cells were maintained in Dulbecco's modified Eagles medium containing 5% foetal calf serum. The soluble TNF α receptor derivatives were transfected into monkey COS cells by means of Lipofectin (GIBCO-BRL, Bethesda MD) according to the manufacturers protocol and cell free supernatants harvested 72 hours post transfection.

Inhibition of TNF α activity

The soluble TNF α receptor derivatives were analyzed for inhibition of TNF α cytotoxic activity in vitro. The cytotoxicity assay was performed as described on the TNF α sensitive cell line WEHI 164 clone 13. Serial dilutions of supernatants from COS cells transfected with the mutant receptors or mock transfected controls were incubated with a constant amount of TNF (1 ng/ml) for 1 hour at 37°C before addition to the assay.

2. RESULTS

In order to understand more about the contribution of

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th individual cyst ine rich subdomains to th binding of TNF α by the solubl form of the 55kD TNF recept r, we removed each subdomain by PCR mutagenesis (Figure 5). COS cells were transfected with each of these constructs and 5 the supernatants were assayed for their ability to inhibit the cytotoxic activity of TNF α . Figure 12 panel A shows that conditioned medium from COS cells tranfected with pTNFRecd inhibits TNF α as previously described. Removal of 10 the fourth cysteine rich subdomain resulted in a protein which, similar to TNFRecd, was a potent inhibitor of TNF α (Figure 12 panel B). The mutants lacking the first, second and third subdomains did not show any inhibitory activity 15 in the TNF α cytotoxicity assay.

EXAMPLE 2: Expression of polypeptide consisting essentially of the first three cysteine-rich subdomains of the extracellular binding domain of the 75kD receptor.

The coding region of the human 75kD TNF α receptor was isolated from a T cell lambda ZAP library, using a probe based on published sequences (3) and cloned into the EcoRI 20 site of a mammalian cell expression vector (12) resulting in plasmid p75TNFR. In more detail, RNA was extracted from a cell line expressing the 75kD receptor and reverse transcribed. Any cell line expressing this receptor could be used, such as those described by Smith *et al* (3). The 25 product of the reverse transcription was subjected to 25 cycles of PCR using the following primers:

5' CGC AGA ATT CCC CGC AGC CAT GGC GCC CGT CGC C 3'
and 5' GTA AGG ATC CTA TCG CCA GTG CTC CCT TCA GCT 3'.

These primers are directed against the extracellular 30 binding domain coding region of the 75kD receptor and were taken from Smith *et al* (3). The amplified product was gel purified and shown to encode TNFR. This was subsequently used to screen the library. Plaque purification was performed ssentially as described in th Referenc Exampl

- 20 -

exc pt that the prob was lab lled by random priming (21) and hybridised in 50% formamid . Filters were washed in 0.2 x SSC (Standard Saline Citrate) twice at 60°C.

A derivative of the 75kD TNF α receptor was produced by 5 engineering a termination codon just prior to the transmembrane domain. Referring to Figure 13, the polymerase chain reaction (PCR) technique was used to generate a 274 bp restriction fragment containing a BglII site at the 5' end and an Xba I site preceded by a TAG stop 10 codon at the 3' end. The PCR primers were 5' ACACGACTTCATCCACGGATA and 5'ACGTTCTAGACTAGTCGCCAGTGCTCCCTTCAGCTG. The PCR product was digested with Bgl II and Xba I, gel purified and cloned into the TNF receptor expression plasmid (described above) 15 digested with BglII and Xba I. DNA sequencing confirmed that the resulting plasmid contained the designed DNA sequence.

A similar approach was utilised to generate a construct which lacked the fourth cysteine-rich subdomain of the 75kD 20 TNF α receptor. PCR was performed using a primer upstream of the Esp I site in the 75kD TNFR and a primer which introduced a TAG termination codon and an Xba I site. The sequences of the primers was 5' CAG AAC CGC ATC TGC ACC TGC and 5'ACGTTCTAGACTTGCACACCACGTCTGATGTTTC respectively. The 25 PCR product was digested with EspI and Xba I and the 110bp DNA fragment gel purified and cloned into Esp I Xba I digested p75TNFR.

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CLAIMS

1. A polypeptide which is capable of binding human TNF α and which consists essentially of:
 - (a) the first three cysteine-rich subdomains, but not the 5 fourth cysteine-rich subdomain, of the extracellular binding domain of the 55kD or 75kD receptor for human TNF α ;
 - or
 - (b) an amino acid sequence having a homology of 90% or more with the said sequence (a).
- 10 2. A polypeptide according to claim 1, which consists essentially of the first three cysteine-rich subdomains of the extracellular binding domain of the 55kD receptor for human TNF α .
- 15 3. A polypeptide according to claim 2, which has the amino acid sequence: M G L S T V P D L L L P L V L L E L V G I Y P S G V I G L V P H L G D R E K R D S V C P Q G K Y I H P Q N N S I C C T K C H K G T Y L V N D C P G P G Q D T D C R E C E S G S F T A S E N 20 H L R H C L S C S K C R K E M G Q V E I S S C T V D R D T V C G C R K N Q Y R H Y W S E N L F Q C F N C S L C L N G T V H L S C Q E K Q N T V C T.
- 25 4. A DNA sequence which encodes a polypeptide as defined in any one of the preceding claims.
5. A DNA sequence according to claim 4, which comprises:
GTG TGT CCC CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT TCG ATT
TGC TGT ACC AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC TGT
30 CCA GGC CCG GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC GGC
TCC TTC ACC GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC
TCC AAA TGC CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC
ACA GTG GAC CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC
CGG CAT TAT TGG AGT GAA AAC CTT TTC CAG TGC TTC AAT TGC AGC

- 24 -

CTC TGC CTC AAT GGG ACC GTG CAC CTC TCC TGC CAG GAG AAA CAG AAC ACC GTG TGC.

6. A DNA sequence according to claim 4 or 5, which further comprises a 5' sequence which encodes a signal 5 amino acid sequence.

7. A DNA sequence according to claim 4, which is:

ATG GGC CTC TCC ACC GTG CCT GAC CTG CTG CTG CCG CTG GTG CTC
CTG GAG CTG TTG GTG GGA ATA TAC CCC TCA GGG GTT ATT GGA CTG
GTC CCT CAC CTA GGG GAC AGG GAG AAG AGA GAT AGT GTG TGT CCC
10 CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT TCG ATT TGC TGT ACC
AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC TGT CCA GGC CCG
GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC GGC TCC TTC ACC
GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC TCC AAA TGC
CGA AAG GAA ATG GGT CAG GTG GAG ATC TT TCT TGC ACA GTG GAC
15 CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC CGG CAT TAT
TGG AGT GAA AAC CTT TTC CAG TGC TTC AAT TGC AGC CTC TGC CTC
AAT GGG ACC GTG CAC CTC TCC TGC CAG GAG AAA CAG AAC ACC GTG
TGC ACC.

8. A vector which incorporates a DNA sequence as 20 claimed in any one of claims 4 to 7 and which is capable, when provided in a suitable host, of expressing the said polypeptide.

9. A vector according to claim 8, which is a plasmid.

25 10. A host transformed with a vector as claimed in claim 8 or 9.

11. A host according to claim 10, which is a mammalian cell line.

12. A process for the preparation of a polypeptide as 30 defined in claim 1, which process comprises culturing a transformed host as claimed in claim 10 or 11 under such conditions that the said polypeptide is expressed.

13. A pharmaceutical composition comprising a pharmaceutically acceptable carrier or diluent and, as an

- 25 -

active principle, a polypeptid as claimed in claim 1.

14. A polypeptide as defined in claim 1 for use in
the treatment of rheumatoid arthritis.

Fig. 1.

1 ACCA GTGATCTCTA TGCCTGAGTC TCAACCCCTCA ACTGTCAACCC CAAGGCACATT GGGACGTCTT GGACAGACCG
 75 AGTCCCCGGGA AGCCCCAGCA CTGCGCTGC CACACTGCCG TGAGCCAAA TGAGGGAGTG AGAGGCCATA GCTGCTGCC

40	M	G	L	S	T	V	P	D	L	L	P	L	V	L	E	L	L	V	G	I	Y	P		
156	ATG	GGC	CTC	TCC	ACC	GTC	CCT	GAC	CTG	CTG	CTG	CTG	GAG	CTG	CTG	CTG	CTG	GAG	CTG	ATA	TAC	CCC		
16	S	G	V	I	G	L	V	P	H	L	G	D	R	E	K	R	D	S	V	C	P	Q	K	
228	TCA	GGG	GTT	ATT	GGA	CTG	GTC	CCT	CAC	CTA	GGG	GAC	AGG	GAG	AAG	AGA	GAT	AGT	GTC	TGT	CCC	CAA	GGG	AAA
9	Y	I	H	P	Q	N	N	S	I	C	C	T	K	C	H	K	G	T	Y	L	Y	N	D	C
300	TAT	ATC	CAC	CCT	CAA	AAT	AAT	TCG	ATT	TGC	TGT	ACC	AAG	TGC	CAC	AAA	GGA	ACC	TAC	TTG	TAC	AAT	GAC	TGT
33	P	G	P	G	Q	D	T	D	C	R	E	C	E	S	G	S	F	T	A	S	E	N	H	L
372	CCA	GGC	CCG	GGG	CAG	GAT	ACG	GAC	TGC	AGG	GAG	TGT	GAG	AGC	GGC	TCC	TTC	ACC	GCT	TCA	GAA	AAC	CAC	CTC
57	R	H	C	L	S	C	S	K	C	R	K	E	M	G	Q	V	E	I	S	S	C	T	V	D
444	AGA	CAC	TGC	CTC	AGC	TGC	TCC	AAA	TGC	CGA	AAG	GAA	ATG	GGT	CAG	GTG	GAG	ATC	TCT	TCT	TGC	TCA	GTG	GAC
81	R	D	T	V	C	G	C	R	K	N	Q	Y	R	H	Y	W	S	E	N	L	F	Q	C	F
516	CGG	GAC	ACC	GTC	TGT	GGC	TGC	AGG	AAG	AAC	CAG	TAC	CGG	CAT	TAT	TGG	ACT	GAA	AAC	CCT	TTC	CAG	TGC	TTC
105	N	C	S	L	C	L	N	G	T	V	H	L	S	C	Q	E	K	Q	N	T	V	C	T	C
558	AAT	TGC	AGC	CTC	TGC	CTC	AAT	GGG	ACC	GTG	CAC	CTC	TCC	TGC	CAG	GAG	AAA	CAG	AAC	ACC	GTG	TGC	ACC	TGC
129	H	A	G	F	F	L	R	E	N	E	C	V	S	C	S	N	C	K	K	S	L	E	C	T
660	CAT	GCA	GGT	TTC	TTT	CTA	AGA	GAA	AAC	GAG	TGT	GTC	TCC	TGT	AGT	AAC	TGT	AAG	AAA	AGC	CTG	GAG	TGC	ACG
153	K	L	C	L	P	Q	I	E	N	V	K	G	T	E	D	S	G	T	T	V	L	L	P	L
732	AAG	TTC	TGC	CTA	CCC	CAG	ATT	GAG	AAT	GTT	AAG	GGC	ACT	GAG	GAC	TCA	GGC	ACC	ACA	GTG	CTG	TTG	CCC	CTG
177	V	I	F	F	G	L	C	L	L	S	L	L	F	I	G	L	M	Y	R	X	Q	R	W	K
804	GTC	ATT	TTC	TTT	GGT	CTT	TGC	CTT	TTA	TCC	CTC	CTC	TTC	ATT	GGT	TTA	ATT	GTC	TAC	TAC	CAA	CGG	TGG	AAG
201	S	K	L	Y	S	I	V	C	G	K	S	T	P	E	K	E	G	E	L	E	G	T	T	T
876	TCC	AAG	CTC	TAC	TCC	ATT	GTT	TGT	GGG	AAA	TCG	ACA	CCT	GAA	AAA	GAG	GGG	GAG	CTT	GAA	GGG	ACT	ACT	ACT

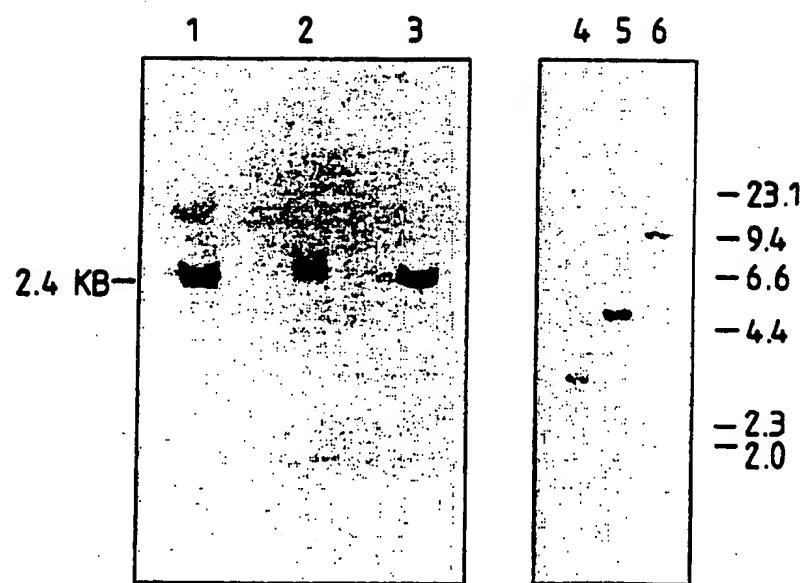
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Fig. 1 (cont.)

225 K P L A P N P S F S P T P G F T P T L G F S P V
 948 AAG CCC CTG GCC CCA AAC CCA AGC TTC AGT CCC ACT CCA GGC TTC ACC CCC ACC CTC GGC GGC TTC AGT CCC CCC GTC
 249 P S S T F T S S S T Y T P G D C P N F A A P R R
 1020 CCC AGT TCC ACC TTC ACC TCC AGC TCC ACC TAT ACC CCC GGT GAC TGT CCC AAC TTT GCG GCT CCC CGC AGA
 273 E V A P P Y Q G A D P I L A T A L A S D P I P N
 1092 GAG GTG GCA CCA CCC TAT CAG GGG GCT GAC CCC ATC CTT GCG GCC CTC GCC TCC GAC CCC ATC CCC AAC
 297 P L Q K W E D S A H K P Q S L D T D D P A T L Y
 1164 CCC CTT CAG AAG TGG GAG GAC ACT GAT GAC CCC AGC CTA GAC ACT GAT GAC CCC GCG ACG CTG TAC
 321 A V V E N V P P L R T L E F V R R L G L S D H E
 1236 GCC GTG GTG GAG AAC GTG CCC CCG TTT CGC TGG AAG GAA TTC GTC CGG CGC CTA GGG CTG AGC GAC CAC GAG
 345 I D R L E L Q N G R C L R E A Q Y S M L A T W R
 1308 ATC GAT CGG CTG GAG CTG CAG AAC GGG CGC TGC CTG CGC GAG GCG CAA TAC AGC ATG CTG GCG ACC TGG AGG
 369 R R T P R R E A T L E L G R V L R N M D L L G
 1380 CGG CGC ACG CCG CGG CGC GAG GCC ACG CTG GAG CTG CTG CGA CGG GTG CTC CGC GAC ATG GAC CTG CTG GGC
 393 C L E D I E E A L C G P A A L P P A P S L L R
 1452 TGC CTG GAG GAC ATC GAG GAG GCG CTT TGC GGC CCC GCG CTC CGG CCC AGT CTT CTC AGA TGA
 1521 GGC TGG CCC TGG GGC AGC TCT AAG GAC GTC CTG CAG ATCG CCT TCC AACC CACTT TTT TCT GGAA AGG AGG GGT C
 1601 CTG CAG GGC AAG CAG GGC TAG CAG GGC CTACT TGG TG CTA ACC CTC GAT GT TAC ATA GCT TTT TCA GGT GCT GGC
 1681 CGC CGC GAC AGT CAG GGC GTG GGC AGA GAG GT C GCG TGG CCT GAG AGC CTG AGT GGG GGT TTG CG GAG GAT
 1761 GAG GAG GCT ATG CCT CATG CCC GTT TTG GTG CCT CAC CAG CAAG GCT GCT CGG GGC CCCT GG TCG TCA GGC
 1841 TTT TCA AG TGC AT AAG CA GTT TTT TTT GTT TGT TTT TGT TAA TCA AT CAG TGT TAC TAA TATA
 1921 GAA ACT TGG C ACT CCT GTG C CCT CTG CCT GAG AGC TGT CCT GAG CCT GAG CCT GAG CCT GAG CCT GAG CCT GAG
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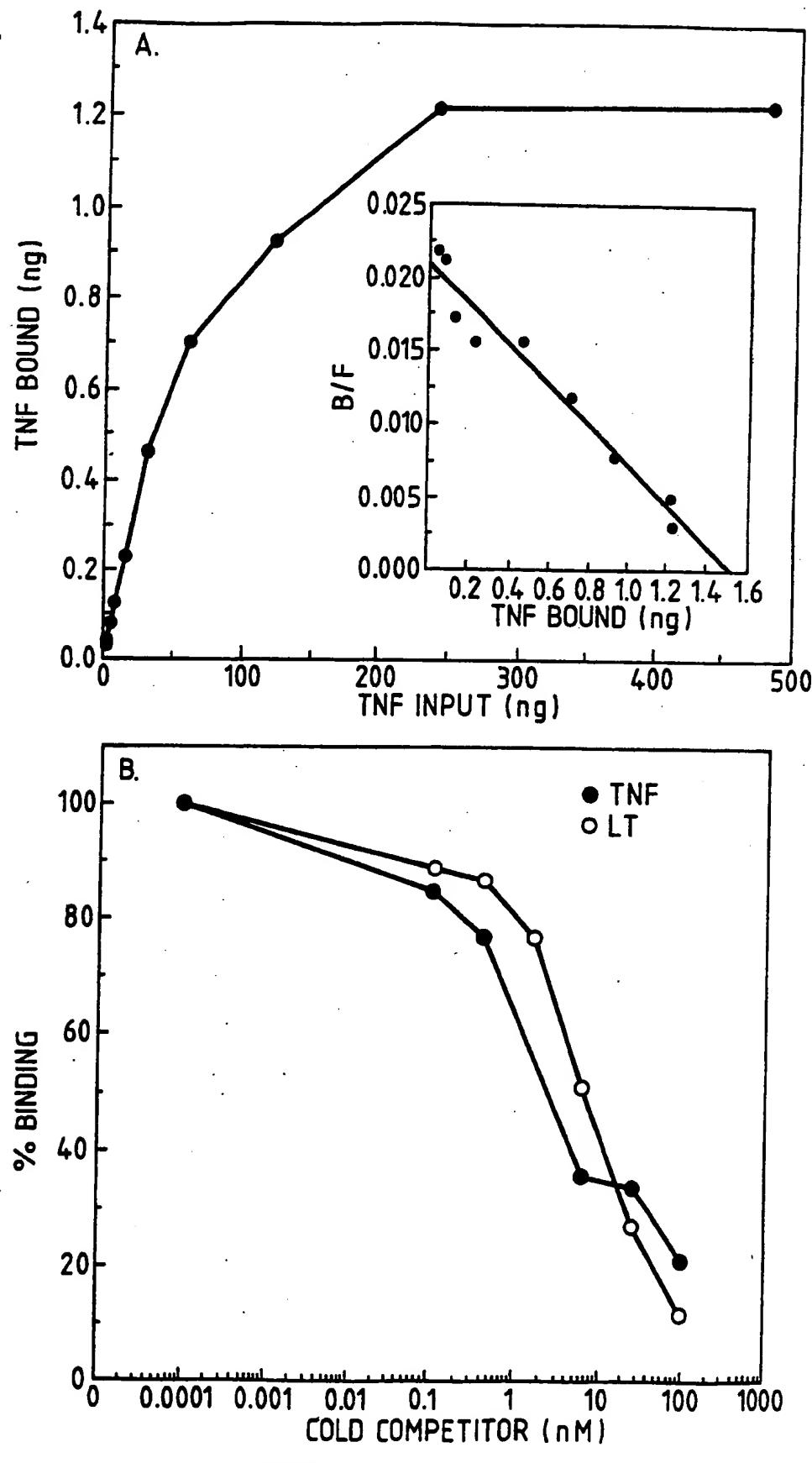
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Fig. 2.



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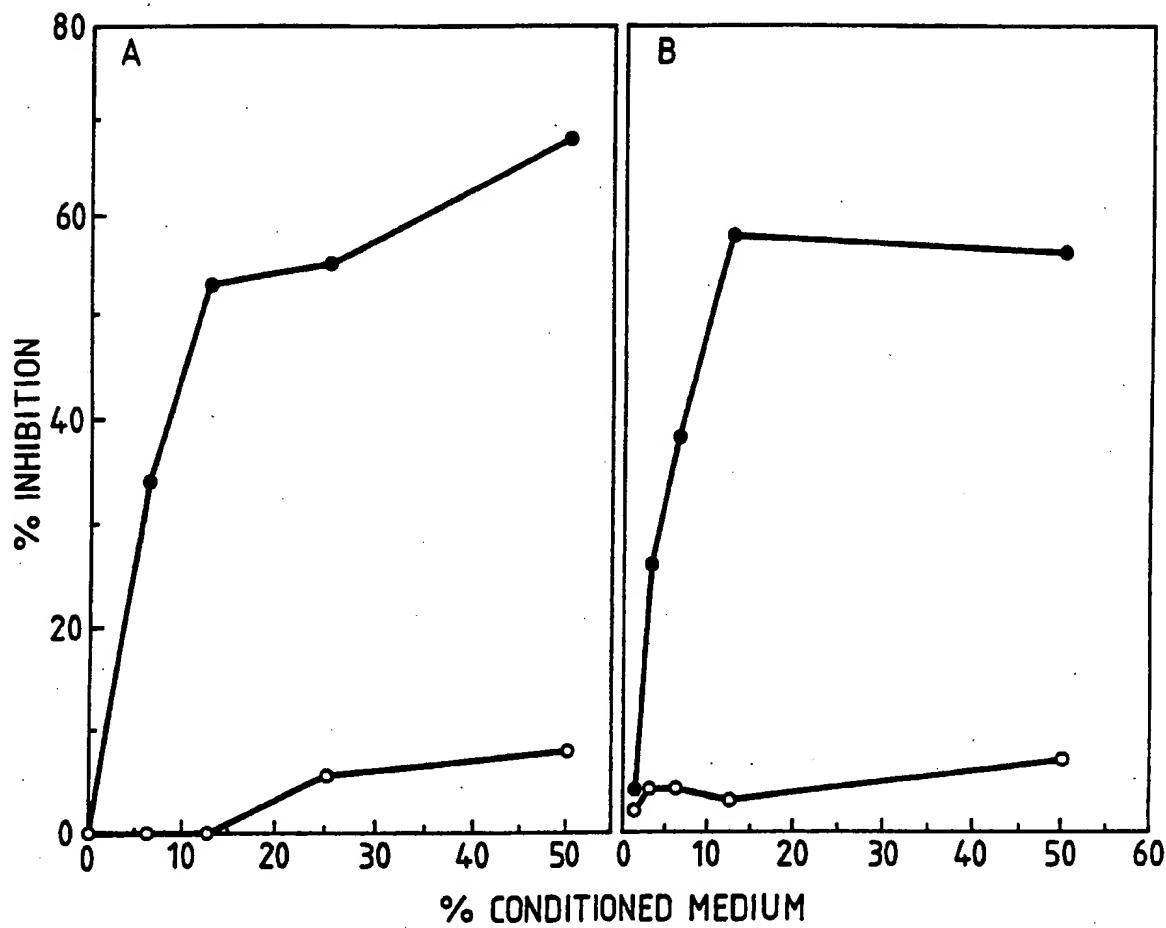
Fig. 3.



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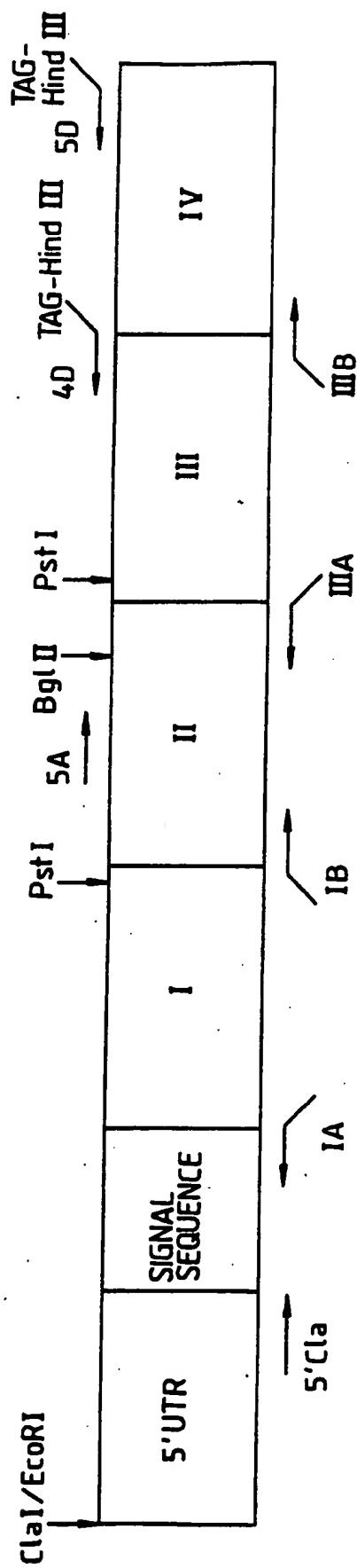
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Fig. 4.



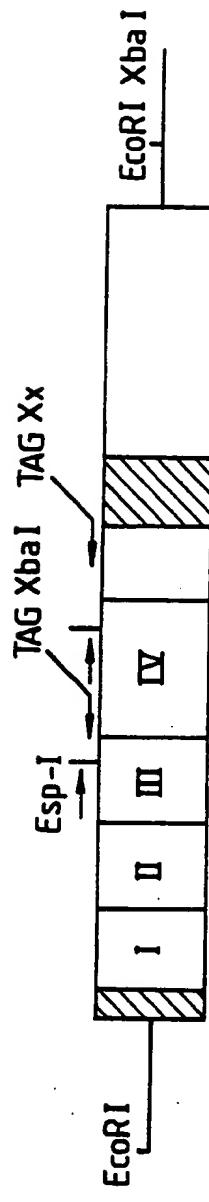
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Fig. 5.



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Fig. 13.



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Fig. 6.

First Subdomain

TNFR-55,
TNFR-75,
NGFR,
CD40,
OX40.

Y	C	P	Q	G	K	Y	!	H	P	Q	N	N	S	!	C	C	I	K	C	H	K	G	I	Y	!	L	Y	N	D	C	P	G	P	Q	D	T	D	C	R			
T	C	A	L	R	E	Y	Y	D	-	Q	T	A	Q	M	-	C	C	S	K	C	S	P	G	H	A	K	V	F	C	T	K	T	S	-	D	T	V	C	D			
T	C	S	T	G	L	Y	T	H	-	-	S	G	E	C	C	-	C	C	K	A	C	N	L	G	E	G	V	A	O	P	C	-	G	A	N	Q	-	T	V	C	E	
A	C	R	E	K	O	Y	L	-	-	-	N	S	Q	C	C	-	N	S	C	L	C	Q	P	Q	K	L	V	S	D	C	T	E	F	T	-	E	T	E	C	L		
N	C	V	K	D	T	Y	P	S	-	-	G	H	K	C	R	-	G	H	K	C	R	E	C	Q	P	G	H	M	V	S	R	C	D	H	T	R	-	D	T	V	C	H

Second Subdomain

TNFR-55,
TNFR-75,
NGFR,
CD40,
OX40.

E	C	-	E	S	G	S	F	T	A	S	E	N	H	L	R	H	C	L	S	C	-	S	K	C	R	K	E	M	G	O	V	E	!	S	S	C	T	V	D	R	D	T	V	C
S	C	-	E	D	S	T	Y	T	T	Q	L	W	N	W	V	P	E	C	L	S	C	-	S	S	D	O	V	E	T	O	A	C	T	R	E	Q	N	R	I	C				
P	C	L	D	N	V	T	F	S	D	V	Y	S	A	T	E	P	C	K	P	C	-	T	E	C	-	L	G	L	O	S	M	S	A	P	C	V	E	A	D	D	A	V	C	
P	C	G	E	S	E	F	L	D	T	W	N	R	E	-	T	H	C	H	Q	H	-	K	Y	C	D	P	N	L	G	R	V	Q	Q	K	G	T	S	E	T	D	T	I	C	
P	C	-	E	P	G	F	Y	N	E	A	V	N	Y	-	D	T	C	K	Q	C	-	T	Q	C	-	H	R	S	G	S	E	L	K	Q	N	T	P	T	E	D	T	V	C	

Third Subdomain

TNFR-55,
TNFR-75,
NGFR,
CD40,
OX40.

G	C	R	K	N	Q	Y	R	H	Y	W	S	E	N	L	F	Q	C	F	N	C	S	L	-	C	L	N	G	I	-	V	H	L	S	Q	E	K	N	T	V	C	
T	C	A	P	G	W	Y	C	A	L	S	K	-	Q	E	G	C	R	C	A	P	L	R	K	C	A	P	G	F	G	Y	A	R	P	G	T	E	S	D	V	V	C
R	C	A	Y	G	Y	Q	D	E	E	T	-	-	G	H	C	E	A	C	S	V	-	C	E	Y	G	S	G	L	V	F	S	C	D	K	O	N	T	V	C		
T	C	E	E	G	W	H	C	T	S	E	A	-	-	-	C	E	S	C	V	L	H	R	S	C	P	G	F	G	V	K	Q	I	A	T	G	V	S	D	T	I	C

Fourth Subdomain

TNFR-55,
TNFR-75,
NGFR,
CD40,
OX40.

T	C	H	A	G	F	F	L	R	E	N	-	-	E	C	V	S	C	S	N	K	K	S	L	E	C	T	K	L	C	L	P	Q	I	E	N	V	K	G	T		
P	C	A	P	G	T	F	S	N	T	S	T	D	I	C	R	P	Q	T	C	N	-	V	V	A	-	V	V	A	I	P	G	N	A	S	M	D	A	V	C		
E	C	P	E	G	T	Y	S	D	E	A	N	H	V	D	P	C	L	P	C	T	V	C	E	D	T	E	R	Q	L	R	E	C	T	P	W	A	-	D	A	E	C
P	C	P	V	G	F	S	N	V	S	S	A	F	E	K	C	H	P	W	T	S	C	E	T	K	D	L	V	Q	O	A	G	T	N	K	T	D	V	C	G		
P	C	P	G	H	F	S	P	G	S	N	Q	-	-	A	C	K	P	W	T	N	C	T	L	S	G	K	Q	I	R	H	P	A	S	N	L	D	T	V	C		

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Fig. 7.

DNA	sequence	608 b.p.	TGTCTGGCATGG	CCCCAGGATTAG	linear
9	/	1			39	/ 11
ATG	GGC	CTC	TCC	ACC	GTG	CCT
met	gly	leu	ser	thr	val	pro
69	/	21	pro	asp	leu	leu
GGG	ATA	TAC	CCC	TCA	GGG	GTT
gly	ile	tyr	pro	ser	gly	val
129	/	41	ile	gly	leu	val
GAT	AGT	GTG	TGT	CCC	CAA	GGG
asp	ser	val	cys	pro	glu	lys
189	/	61	lys	tyr	ile	his
MAG	TGC	CAC	AAA	GGA	ACC	TAC
lys	cys	his	lys	gly	thr	tyr
249	/	81	lys	thr	tyr	leu
TGC	AGG	GAG	TGT	GAG	AGC	GGC
cys	arg	glu	cys	glu	ser	gly
309	/	101	ser	gly	ser	thr
AGC	TGC	TCC	AAA	TGC	CGA	AAG
ser	cys	ser	lys	cys	arg	lys
369	/	121	lys	glu	met	gly
CGG	GAC	ACC	GTG	TGT	GGC	TGC
arg	asp	thr	val	cys	gly	cys
429	/	141	lys	arg	cys	arg
TTC	CAG	TGC	TTC	AAAT	TGC	CTC
phe	gln	cys	phe	asn	cys	lys
489	/	161	asn	cys	ser	leu
AAA	CAG	AAC	ACC	GTG	TGC	ACC
lys	gln	asn	thr	val	cys	thr
549	/	181	thr	cys	lys	lys
TCC	TGT	AGT	AAC	TGT	AAG	AAA
ser	cys	ser	asn	cys	lys	lys
			ser	lys	ser	leu
			leu	cys	thr	lys
			lys	leu	glu	lys
			leu	cys	thr	lys
			leu	pro	gln	ile
			leu	pro	gln	ile
			leu	pro	gln	ile

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Fig. 8.

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Fig. 9.

DNA sequence 470 b.p. TGTCTGGCATGG . . . CCCAGAGATTAG linear

9 / 1	ATG GGC CTC RCC ACC GTG CCT GAC CTG CTG CTC CCG	CTG GAG CTC CTC GCG CTC CTC GAG CTG TTG GRG
met gly leu ser thr val pro asp leu leu leu pro leu val leu glu leu leu leu val	69 / 21	99 / 31
GGA ATA TAC CCC TCA GGG GRT ATT GGA CTG GTC CCT CAC CTA GGG GAC AGG GAG AAG AGA	91	
gly ile tyr pro ser gly val ile gly leu val pro his leu gly asp arg glu lys arg	129 / 41	159 / 51
GAT AGT GTG TGT CCC CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT TCG ATT TGC TGT ACC	189 / 61	219 / 71
asp ser val cys pro gln gly lys tyr ile his pro gln asn ser ile cys cys thr		
AAG TGC CAC AAA GGA ACC TAC TTG TAC ATT GAC TGT CCA GGC CCG GGG CAG GAT ACG GAC		
lys cys his lys gly thr tyr leu tyr asp cys pro gly pro gln asp thr asp	249 / 81	279 / 91
TGC AGG AAG AAC CAG TAC CGG CAT TAT TGG AGT GAA AAG CTT TTC CAG TGC TTC ATT TGC		
cys arg lys asn gln tyr arg his tyr trp ser glu asn leu phe gln cys phe asn cys	309 / 101	339 / 111
AGC CTC TGC CRC AAT GGG ACC GTG CAC CTC TCC TGC CAG GAG AAA CAG AAC ACC GTG TGC		
ser leu cys leu asn gly thr val his leu ser cys gln glu lys gln asn thr val cys	369 / 121	399 / 131
ACC TGC CAT GCA GGT TTC TTT CTA AGA GAA AAC GAG TGT GTC TCC TGT AGT AAC TGT AAG		
thr cys his ala gly phe leu arg glu asn glu cys val ser cys ser asn cys lys	429 / 141	459 / 151
AAA AGC CTG GAG TGC ACG AAG TTG TGC CTA CCC CAG ATT TAG		
lys ser leu glu cys thr lys leu cys leu pro gln ile AMB		

SUBSTITUTE SHEET

Fig. 10.

DNA sequence	485 b.p.	TGTCTGGCATGG . . . CCCCAGATTAG	linear
9 / 1	39 / 11		
ATG GGC CTC TCC ACC GTG CCT GAC CTG CTG CTC GTC CCG CTC GAG CTC CTG GAG	ATG GTC CTC GTC		
met gly leu ser thr val pro asp leu leu leu pro leu val leu glu leu leu val	met gly leu ser thr val pro leu val leu glu leu leu val		
69 / 21	99 / 31		
GCA ATA TAC CCC TCA GGG GTT ATT GGA CTG GTC CCT CAC CTA GGG GAC AGG GAG AAG			
gly ile tyr pro ser gly val ile gly leu val pro his leu gly asp arg glu lys arg			
129 / 41	159 / 51		
GAT AGT GTG TGT CCC CCA GGA AAA TAT ATC CAC CCT CAA AAT ATT TCG ATT TGC TGT ACC			
asp ser val cys pro gln gly lys tyr ile his pro gln asn ser ile cys cys thr			
189 / 61	219 / 71		
AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC TGT CCA GGC CCG GGG CAG GAT ACG GAC			
lys cys his lys gly thr tyr leu tyr asp asp cys pro gly pro gln asp thr asp			
249 / 81	279 / 91		
TGC AGG GAG TGT GAG AGC GGC TCC TTC ACC GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC			
cys arg glu cys glu ser gly ser phe thr ala ser glu asn his leu arg his cys leu			
309 / 101	339 / 111		
AGC TGC TCC AAA TGC CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC ACA GTG GAC			
ser cys ser lys cys arg lys glu met gly gln val glu ile ser ser cys thr val asp			
369 / 121	399 / 131		
CGG GAC ACC GTG TGT ACC TGC CAT GCA GGT TTC TTT CTA AGA GAA AAC GAG TGT GTC TCC			
arg asp thr val cys thr cys his ala gly phe leu arg glu asn glu cys val ser			
429 / 141	459 / 151		
TGT AGT AAC TGT AAG AAA AGC CTC GAG TGC ACG AAG RTG TGC CTA CCC CAG ATT TAG			
cys ser asn cys lys lys ser leu glu cys thr lys leu pro gln ile AMB			

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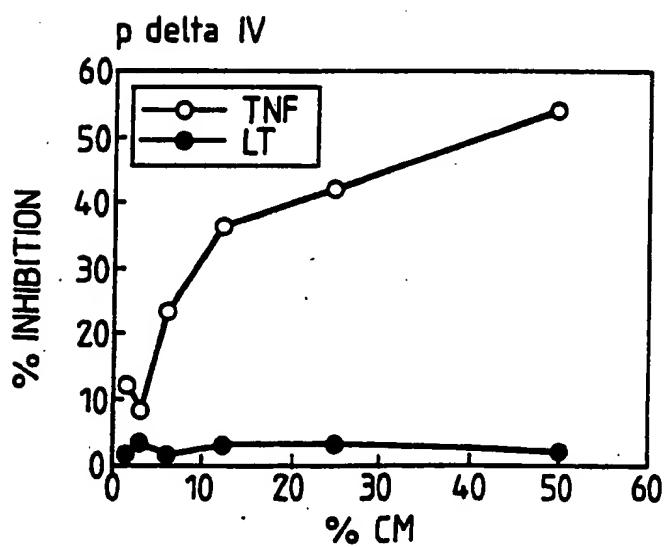
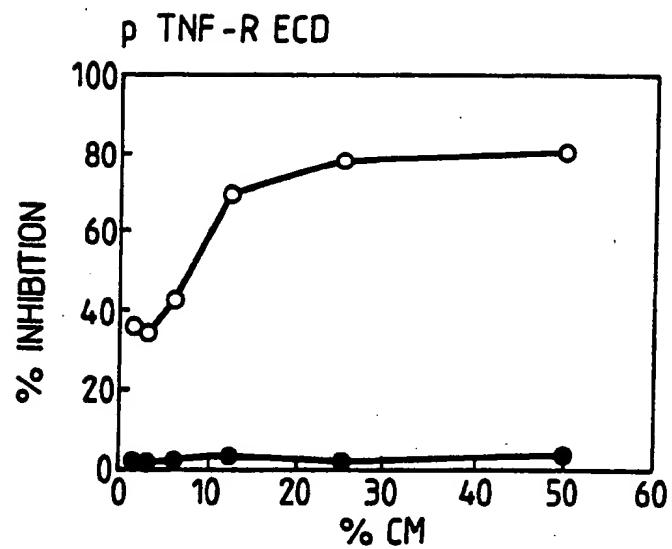
Fig. 11.

DNA sequence 512 b.p. TGTCTGGATGG ... GTGTGACCTGTA linear

9 / 1	ATG GGC CTC TCC ACC GTC GCG CCT GAC CTG CTG CCG CTG CTG CTC CTC GAG CTC GAG CTC GAG	39 / 11	met gly leu ser thr val pro asp leu leu leu pro leu val leu glu leu leu val
69 / 21	GGG ATA TAC CCC TCA GGG GTT ATT GGA GTC CCT CAC CTC CTA GGG GAC AGG GAG AGA	99 / 31	gly ile tyr pro ser gly val ile gly leu val pro his leu gly asp arg glu lys arg
129 / 41	GAT AGT GTC TGT CCC CAA GGA AAA TAT ATC CAC CCT CAA AAT ATT TCG ATT TGC TGT ACC	159 / 51	asp ser val cys pro gln gly lys tyr ile his pro gln asn ser ile cys cys thr
189 / 61	AAG TGC CAC AAA GGA ACC TAC TAC ATT GAC TGT CCA GGC CCG GGG CAG GAT ACG GAC	219 / 71	lys cys his lys gly thr tyr leu tyr asp cys pro gly pro gly gln asp thr asp
249 / 81	TGC AGG GAG TGT GAG AGC GGC TCC TTC ACC GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC	279 / 91	cys arg glu cys glu ser gly ser phe thr ala ser glu asn his leu arg his cys leu
309 / 101	AGC TGC TCC AAA TGC CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC ACA GTG GAC	339 / 111	ser cys ser lys cys arg lys glu met gln val glu ile ser ser cys thr val asp
369 / 121	CGG GAC ACC GTG TGT GGC TGC AGG AAC CAG TAC CGG CAT TAT TGG AGT GAA AAC CTT	399 / 131	arg asp thr val cys gly cys arg lys asn gln tyr arg his tyr trp ser glu asn leu
429 / 141	TTC CAG TGC TTC ATT TGC AGC CTC TGC CTC AAT GGG ACC GTG CAC CTC TCC TGC CAG GAG	459 / 151	phe gln cys phe asn cys ser leu cys leu asn gln thr val his leu ser cys gln glu
489 / 161	AAA CAG AAC ACC GTC TGC ACC TGA		lys gln asn thr val cys thr GPA

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Fig. 12.



INTERNATIONAL SEARCH REPORT

International Application No.

PCT/GB 91/01826

I. CLASSIFICATION OF SUBJECT MATTER (If several classification symbols apply, indicate all)⁶

According to International Patent Classification (IPC) or to both National Classification and IPC

Int.Cl. 5 C12N15/12; C07K13/00; A61K37/02

II. FIELDS SEARCHED

Minimum Documentation Searched⁷

Classification System	Classification Symbols
Int.Cl. 5	C07K

Documentation Searched other than Minimum Documentation
to the Extent that such Documents are Included in the Fields Searched⁸III. DOCUMENTS CONSIDERED TO BE RELEVANT⁹

Category ¹⁰	Citation of Document, ¹¹ with indication, where appropriate, of the relevant passages ¹²	Relevant to Claim No. ¹³
X	EP, A, 0 308 378 (YEDA RESEARCH AND DEVELOPMENT COMPANY, LIMITED) 22 March 1989 see the whole document ----	1-14
X	CELL. vol. 61, 20 April 1990, CAMBRIDGE, MA US pages 351 - 359; Shall, T.J. et al.: 'Molecular cloning and expression of the human 55Kd tumor necrosis factor receptor.' see the whole document ----	1-14
X	CELL. vol. 61, 20 April 1990, CAMBRIDGE, MA US pages 361 - 370; Loetscher, H. et al.: 'Molecular cloning and expression of a receptor for human tumor necrosis factor.' see the whole document ----	1-14

¹⁰ Special categories of cited documents :¹⁰

- ^{"A"} document defining the general state of the art which is not considered to be of particular relevance
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- ^{"D"} document referring to an oral disclosure, use, exhibition or other means
- ^{"E"} document published prior to the international filing date but later than the priority date claimed

- ^{"F"} later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- ^{"G"} document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step
- ^{"H"} document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
- ^{"I"} document member of the same patent family

IV. CERTIFICATION

Date of the Actual Completion of the International Search

2

23 JANUARY 1992

Date of Mailing of this International Search Report

06.02.92

International Searching Authority

EUROPEAN PATENT OFFICE

Signature of Authorized Officer

NAUCHE S.A.

III. DOCUMENTS CONSIDERED TO BE RELEVANT (CONTINUED FROM THE SECOND SHEET)		
Category *	Citation of Document, with indication, where appropriate, of the relevant passages	Relevant to Claim No.
X	PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA. vol. 87, 1 October 1990, WASHINGTON US pages 7380 - 7384; Gray, Patrick W.; Barrett, Kathy; Chantry, David; Turner, Martin; Feldmann, Marc: 'Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of recombinant soluble TNF-binding protein' see the whole document ----	1-14
P,X	EP,A,0 393 438 (BOEHRINGER INGELHEIM INTERNATIONAL) 24 October 1990 see the whole document ----	1-14

ANNEX TO THE INTERNATIONAL SEARCH REPORT
ON INTERNATIONAL PATENT APPLICATION NO. GB 9101826
SA 52300

This annex lists the patent family members relating to the patent documents cited in the above-mentioned international search report. The members are as contained in the European Patent Office EDP file on The European Patent Office is in no way liable for these particulars which are merely given for the purpose of information. 23/01/92

Patent document cited in search report	Publication date		Patent family member(s)	Publication date
EP-A-0308378	22-03-89		AU-A- 2206888 JP-A- 2000200	16-03-89 05-01-90
EP-A-0393438	24-10-90		DE-A- 3913101 DE-A- 3920282 JP-A- 3164179	31-10-90 03-01-91 16-07-91

FIG. 4A

	1		50
huCHD	MPSTPAPPAPLLLEGGLLEEGSRPARAGPEPPVLPIRSEKEPLPVRAAG		
huCHL	---MGGMKYIFSLLEFFLLEEG-----		GKTEQVKHSETY
huCHL2	---MVEPVRVLESSLGLALLWFP-----		LDSHARARPDM
	51		100
huCHD	CTEGGKVVAIDETWHPDLEPEPGVMRCVLCACEAPQWGRTRGPGRVSCK		
huCHL	CMFQDKKIVYRGERWHPYL-EPYGLVYGVNCICSENGNVLCSE-		
huCHL2	CLFHGKRYSPGESWHPYL-EPOGLMYCLRCTCSEGAHVSCYR-----		
	101		150
huCHD	NIKPECPPTPACQPROLPGHCCQTCPOERSSSERQPSGLSFEYPRDPEHR		
huCHL	---VRCENVHCLSPVHILPHLCCPRCPEDSLPPVN---NKVTSKSCEYNG		
huCHL2	---EHCPVHGPQPVTEBQQCCPKGEVEPHTPSG---LRAPPKSCQHNG		
	151		200
huCHD	SYSDRGEPEGAERARGDHTDFVALLTGPRSQAVARARVSLLRSSLRFSI		
huCHL	TTYQHGEIIFVAEGLFQNRQPNQCTQSCSCSEG-----		
huCHL2	TMYQHGEIIFSAHELFPSRLPNQCVLCSCTEG-----		
	201		250
huCHD	SYRRLLDRPTRIRFSDNSGNSVLFEPAPTDGLVCGVWRAPRLSLRLLR		
huCHL	-----NVYCGLKTCPKLTCAFPIVSDSCCRVCRGDG-ELSW		
huCHL2	-----QTYCGLTTCPPEPGCPAPPLPDSCCQACKDEASEQSD		
	251		300
huCHD	AEQLHVALVTETHPSGEVWGPLIRHRLAAETFSALLTLEGPPQQGVGGI		
huCHL	EHSDGDIFRQ PANREARHSYHRSHYDPPPSRQAGGLSRFP-----		
huCHL2	EEDSVQSLHGVVRHPQDPCSSDAGRKRCPGTPAPTGLS-----		
	301		350
huCHD	TLLTLSDTEDSLHFLLLFRGLEEPSSGLTQVPERLQILHOGOLERELOA		
huCHL	-----GARSHRGALMDSQOASGTIVQIVNNKHHGQCVSNG		
huCHL2	-----APLSFIPRHFRPKGAGSTTVKIVLKEHKK--ACVHGG		
	351		400
huCHD	NVSQOEPGEAEVLPNLTVQEMDWLVLGELQMALEWAGRPGLRISGHIAAR		
huCHL	KTYSHGESWHPNLRAFGTIVECVLCTCNVTQECKKIHCPNRYPCKPQK		
huCHL2	KTYSHGEVWHPAFRAFGPEPCILCTCEDGROECQRVTCPTEYPCRHPEKV		
	401		450
huCHD	KSCDVLQSVLCGADALIPVQITGAAGSASLTLLGNGSIIYQVQVVGTSSEV		
huCHL	DGKCCCKCPGKKAKEELPGQSFDNKGYFCGEETMPVYESVFMEDGETRK		
huCHL2	AGKCCCKCP---EDKADPGHSEISSTRCPKAPGRVIEVHTSVSPSPDNLRR		
	451		500
huCHD	VAMTLETKPQRRDQRTILCHMAGLQPGGHTAVGICPGLGARGAHMELQNE		
huCHL	IALETERPPQ-----VEVHWWTIRKG-----ILQHF		
huCHL2	FALEHEASDL-----VEVYWKLVKG-----IFHLT		

FIG. 4B

	501	550
huCHD	LFLNVGTD KDFPD GELRGHVAALPYCGHSARHDTLPVPLAGALVLPPVKSQ	
huCHL	HIEK SKR -MFEELPHFKLVTRTTLSQWK I FTEGEAQISQMCSSRVCRT	
huCHL2	QIKKVRKQDFQKEAQHFR L AGP H EGHWNVFLAQ T ELKV T ASPDKV T KT	
	551	600
huCHD	AAGHAW I SLDTHCHLH Y EVL L AGLGGSEQGT V TAHLLGPPGTPGPR LL K	
huCHL	LEDLV K V L YLERSEK G H C	
huCHL2	-----	
	601	650
huCHD	GFYGSEAQGVVKDLEPELLRHLAKGMA SLL ITTKGS P R G ELRGQVHIANQ	
huCHL	-----	
huCHL2	-----	
	651	700
huCHD	CEVGG L REAAGAEGV V APDTASAAPPV V PGLPALAPAKPGGGPGR PR	
huCHL	-----	
huCHL2	-----	
	701	750
huCHD	DPNTCFEGQQ R PHGARWAPNYDPLCSLCTCQRRTVICDPVV C PPPSCPH	
huCHL	-----	
huCHL2	-----	
	751	800
huCHD	PVQAPDQCCPVCPEKQDV R DL P GL P RSRDPGEGCYFDGDR S WRAAGTRWH	
huCHL	-----	
huCHL2	-----	
	801	850
huCHD	PVVPPFGLIKCAVCTCKGGTGEVHCEKVQC P RLACAQPVRVNPTD C CKQC	
huCHL	-----	
huCHL2	-----	
	851	900
huCHD	PVGSGAHPQLGDP M Q Q SCR F AGQWF P ESQSWHPSV P PF G EMSCITC	
huCHL	-----	
huCHL2	-----	
	901	950
huCHD	RCGAGVPHCERDDCSLPLSCGSGKESRCCSRCTAHRRPAPETRTDPELEK	
huCHL	-----	
huCHL2	-----	
	951	
huCHD	EAEGS	
huCHL	-----	
huCHL2	-----	